

SEQUENCE LISTING

<110> Duvick, Jonathan P.
 Gilliam, Jacob T.
 Maddox, Joyce R.
 Crasta, Oswald R.
 Folkerts, Otto

<120> Amino Polyol Amine Oxidase
 Polynucleotides and Related Polypeptides and Methods of Use

<130> 0875C

<150> US 60/092,936
<151> 1998-07-15

<150> US 09/352,168
<151> 1999-07-12

<160> 33

<170> FastSEQ for Windows Version 3.0

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<213> Exophiala spinifera.

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<222> (346)...(346)
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 attgtcgatc gacgtcgatg ctggatatctc tggcaaatga gatggggtca cagctcgatt 180
 ggaggacgccc cgagaagcct tggccgcaccacggctt gtcccatacg aagactatct 240
 tgctatagta gcccaggata gaattttccg ccaatgcttg cttctcgccg ggaagaggtg 300
 gtgaaaatgt caaggtggg tacaaggttt tcggtaacga aaccancacc ttttgcttc 360
 ggaacacggc gc 372

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 tacaaggttt tcggtaacga aaccaccacc ttttgcttc ggaacacggc gcccggcc 120
 gatcgtaactg tacagccgg tggcgactgc tcaatttcag cgacgggggt gttgaggtgc 180
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<210> 3
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<212> DNA
<213> Artificial Sequence

<220>

<223> Designed oligonucleotide for 3' RACE, N21965

<400> 3
tggtttcgtt accgacaacc ttgtatccc 29

<210> 4
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide for 5' RACE, N21968

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gagttggtcc cagacagact tttgtcgt 28

<210> 5
<211> 1389
<212> DNA
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<222> (1)...(1386)

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gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt 96
Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
20 25 30

gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt 144
Glu Ala Met Asp Arg Val Gly Lys Thr Leu Ser Val Gln Ser Gly
35 40 45

ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac 192
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
50 55 60

agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag 240
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
65 70 75 80

ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac 288
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
85 90 95

ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag 336
Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
100 105 110

gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc 384
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
115 120 125

gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg 432
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
130 135 140

ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg	480
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu	
145 150 155 160	
cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt	528
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly	
165 170 175	
gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag	576
Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys	
180 185 190	
agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg	624
Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly	
195 200 205	
cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg	672
Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met	
210 215 220	
tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct	720
Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala	
225 230 235 240	
gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc	768
Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly	
245 250 255	
gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg	816
Ala Val Phe Arg Ser Lys Lys Val Val Ser Leu Pro Thr Thr Leu	
260 265 270	
tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca	864
Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala	
275 280 285	
ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta	912
Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val	
290 295 300	
tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa	960
Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln	
305 310 315 320	
tcg agc tgt gac ccc atc tca ttt gcc aga gat acc acc agc atc gac gtc	1008
Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val	
325 330 335	
gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg	1056
Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg	
340 345 350	
aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac	1104
Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp	
355 360 365	
caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg	1152
Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro	
370 375 380	
gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga	1200
Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly	

DRAFT

385	390	395	400
gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser 405			
410			
415			
gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr 420			
425			
430			
tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln 435			
440			
445			
cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala 450			
455			
460			
tag			
1389			
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Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly 35 40 45			
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp 50 55 60			
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu 65 70 75 80			
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp 85 90 95			
Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu 100 105 110			
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile 115 120 125			
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg 130 135 140			
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu 145 150 155 160			
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly 165 170 175			
Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys 180 185 190			
Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly 195 200 205			
Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met 210 215 220			
Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala 225 230 235 240			
Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly 245 250 255			
Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu 260 265 270			
Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala 275 280 285			

Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val
 290 295 300
 Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln
 305 310 315 320
 Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val
 325 330 335
 Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg
 340 345 350
 Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp
 355 360 365
 Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro
 370 375 380
 Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly
 385 390 395 400
 Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser
 405 410 415
 Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr
 420 425 430
 Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
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 Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
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<210> 7
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<221> intron
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Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu	
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gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt	144
Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly	
35 40 45	

ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac	192
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp	
50 55 60	

agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag	240
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu	
65 70 75 80	

ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac	288
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp	
85 90 95	

ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag	336
Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu	
100 105 110	
ggt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc	384
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile	
115 120 125	
gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg	432
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg	
130 135 140	
ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg	480
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu	
145 150 155 160	
cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt	528
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly	
165 170 175	
gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag	576
Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys	
180 185 190	
agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg	624
Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly	
195 200 205	
cag tat gtg cga tgc aaa aca g gtgcgtgtgg tgcgtctca ggtgggggac	676
Gln Tyr Val Arg Cys Lys Thr	
210 215	
tcgtttctca gtggcatttc cag gt atg cag tcg att tgc cat gcc atg tca	728
Gly Met Gln Ser Ile Cys His Ala Met Ser	
220 225	
aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa	776
Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu	
230 235 240	
att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc	824
Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala	
245 250 255	
gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat	872
Val Phe Arg Ser Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr	
260 265 270	
ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg	920
Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu	
275 280 285	
gct gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg	968
Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp	
290 295 300 305	
gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg	1016
Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser	
310 315 320	
agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat	1064

Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp			
325	330	335	
cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cg aag			1112
Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys			
340	345	350	
tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac caa			1160
Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln			
355	360	365	
ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc			1208
Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala			
370	375	380	385
aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct			1256
Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala			
390	395	400	
ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg			1304
Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala			
405	410	415	
ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct			1352
Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser			
420	425	430	
tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga			1400
Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg			
435	440	445	
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Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala			
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<213> Exophiala spinifera			
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Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly			
35	40	45	
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp			
50	55	60	
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu			
65	70	75	80
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp			
85	90	95	
Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu			
100	105	110	
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile			
115	120	125	
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg			
130	135	140	
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu			
145	150	155	160

Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
 165 170 175
 Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
 180 185 190
 Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
 195 200 205
 Gln Tyr Val Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met
 210 215 220
 Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala
 225 230 235 240
 Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly
 245 250 255
 Ala Val Phe Arg Ser Lys Lys Val Val Ser Leu Pro Thr Thr Leu
 260 265 270
 Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala
 275 280 285
 Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val
 290 295 300
 Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln
 305 310 315 320
 Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val
 325 330 335
 Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg
 340 345 350
 Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp
 355 360 365
 Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro
 370 375 380
 Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly
 385 390 395 400
 Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser
 405 410 415
 Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr
 420 425 430
 Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
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 Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
 450 455 460

<210> 9
 <211> 458
 <212> PRT
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<400> 9

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 35 40 45
 Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
 50 55 60
 Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
 65 70 75 80
 Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
 85 90 95
 Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
 100 105 110
 Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
 115 120 125
 Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg

130	135	140	
Leu Asp Ser Val Ser Phe Ala His Tyr Cys	Glu Lys Glu Leu Asn Leu		
145	150	155	160
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly			
165	170	175	
Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys			
180	185	190	
Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly			
195	200	205	
Gln Tyr Val Arg Cys Lys Thr Gly Ala Cys Gly Val Val Ser Gly Gly			
210	215	220	
Gly Leu Val Ser Gln Trp Ser Phe Gln Val Cys Ser Arg Phe Ala Met			
225	230	235	240
Pro Cys Gln Arg Asn Leu Phe Gln Ala Gln Cys Thr Ser Thr Pro Pro			
245	250	255	
Ser Leu Lys Leu Ser Ser Arg His Pro Ala Val Gln Tyr Asp Arg Pro			
260	265	270	
Arg Ala Pro Cys Ser Glu Ala Lys Arg Trp Trp Phe Arg Tyr Arg Gln			
275	280	285	
Pro Cys Ile Pro Pro His Phe His His Leu Phe Pro Pro Arg Ser Lys			
290	295	300	
His Trp Arg Lys Ile Leu Ser Trp Ala Thr Ile Ala Arg Ser Ser Tyr			
305	310	315	320
Gly Thr Ser Arg Gly Gly Ala Asn Lys Ala Ser Arg Ala Ser Ser Asn			
325	330	335	
Arg Ala Val Thr Pro Ser His Leu Pro Glu Ile Pro Ala Ser Thr Ser			
340	345	350	
Ile Asp Asn Gly Pro Leu Pro Val Ser Trp Ser Glu Thr Arg Asp Gly			
355	360	365	
Ser Gly Pro Asn Ser Pro Ser Arg Tyr Asp Lys Ser Leu Ser Gly Thr			
370	375	380	
Asn Ser Ala Gln Pro Thr Arg Thr Pro Gly Pro Lys Ser Gln Ser Arg			
385	390	395	400
Pro Thr Cys Ser Lys Ser Ser Gly Arg Ser Ser Ser Ile Ser Lys Glu			
405	410	415	
Leu Arg Ala Pro Ser Met Gly Thr Ile Ser Ser His Trp Val Arg Arg			
420	425	430	
Ser Glu Arg Arg Ser Arg Val Phe Ile Ser Leu Glu Arg Arg Arg Leu			
435	440	445	
Phe Gly Lys Gly Ile Trp Lys Gly Pro Tyr			
450	455		

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 <212> DNA
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<220>
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 <222> (1)...(1389)

<221> misc_feature
 <222> (1)...(3)
 <223> Extra lysine in K:trAPAO

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Lys Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly			
1	5	10	15

48

ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt			
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val			

96

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ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser 35 40 45			144
ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn 50 55 60			192
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu 65 70 75 80			240
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln 85 90 95			288
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu 100 105 110			336
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu 115 120 125			384
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys 130 135 140			432
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn 145 150 155 160			480
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu 165 170 175			528
ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile 180 185 190			576
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly 195 200 205			624
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala 210 215 220			672
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val 225 230 235 240			720
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser 245 250 255			768
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr 260 265 270			816

ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln 275 280 285	864
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe 290 295 300	912
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu 305 310 315 320	960
caa tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp 325 330 335	1008
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly 340 345 350	1056
cgx aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp 355 360 365	1104
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu 370 375 380	1152
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln 385 390 395 400	1200
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly 405 410 415	1248
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu 420 425 430	1296
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly 435 440 445	1344
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala 450 455 460	1389
tag	1392
<210> 11	
<211> 463	
<212> PRT	
<213> Exophiala spinifera	
<220>	
<223> Extra lysine in the polypeptide sequence of K:trAPAO, 463 aa.	
<400> 11	
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly 1 5 10 15	

Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
 20 25 30
 Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
 35 40 45
 Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
 50 55 60
 Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
 65 70 75 80
 Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
 85 90 95
 Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
 100 105 110
 Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
 115 120 125
 Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
 130 135 140
 Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
 145 150 155 160
 Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
 165 170 175
 Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
 180 185 190
 Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
 195 200 205
 Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala
 210 215 220
 Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
 225 230 235 240
 Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
 245 250 255
 Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
 260 265 270
 Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
 275 280 285
 Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
 290 295 300
 Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
 305 310 315 320
 Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
 325 330 335
 Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
 340 345 350
 Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
 355 360 365
 Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
 370 375 380
 Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
 385 390 395 400
 Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
 405 410 415
 Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
 420 425 430
 Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
 435 440 445
 Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
 450 455 460

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<210> 12
<211> 34
<212> DNA
<213> Artificial Sequence
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<220>
 <223> Primer sequence designed for cloning DNA into
 expression vectors, N23256

<400> 12
 ggggaattca aagacaacgt tgccggacgtg gtag 34

<210> 13
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer sequence designed for cloning DNA into
 expression vectors, N23259

<400> 13
 ggggcggccg cctatgctgc tggcaccagg ctag 34

<210> 14
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide for 3' RACE, N21965

<400> 14
 tggtttcgtt accgacaacc ttgtatccc 29

<210> 15
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide for 5' race, N21968

<400> 15
 gagttggtcc cagacagact tttgtcgt 28

<210> 16
 <211> 1673
 <212> DNA
 <213> Exophiala spinifera

<220>
 <221> sig_peptide
 <222> (1)...(267)
 <223> yeast alpha mating factor secretion signal.

<221> CDS
 <222> (1)...(1662)

<400> 16
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 Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
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gca tta gct gct cca gtc aac act aca aca gaa gat gaa acg gca caa
 Ala Leu Ala Ala Pro Val Asn Thr Thr Glu Asp Glu Thr Ala Gln 96
 -70 -65 -60

att ccg gct gaa gct gtc atc ggt tac tca gat tta gaa ggg gat ttc Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe -55 -50 -45	144
gat gtt gct gtt ttg cca ttt tcc aac agc aca aat aac ggg tta ttg Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu -40 -35 -30	192
ttt ata aat act act att gcc agc att gct gct aaa gaa gaa ggg gta Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val -25 -20 -15 -10	240
tct ctc gag aaa aga gag gct gaa gtc gaa ttc aaa gac aac gtt gcg Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Lys Asp Asn Val Ala -5 1 5	288
gac gtg gta gtg gtc gct ggc ttg agc ggt ttg gag acg gca cgc Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg 10 15 20	336
aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp 25 30 35	384
cgt gta ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr 40 45 50 55	432
act atc aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser 60 65 70	480
gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln 75 80 85	528
agg acg act gga aat tca atc cat caa gca caa gac ggt aca acc act Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr 90 95 100	576
aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala 105 110 115	624
ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser 120 125 130 135	672
ctt caa gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val 140 145 150	720
agc ttc gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu 155 160 165	768
ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His 170 175 180	816
gag atc agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt	864

Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly			
185	190	195	
ctc agt aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga			912
Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg			
200	205	210	215
tgc aaa aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt			960
Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu			
220	225	230	
gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag			1008
Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln			
235	240	245	
tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtc ttc cga			1056
Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg			
250	255	260	
agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg			1104
Ser Lys Lys Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu			
265	270	275	
aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat			1152
Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn			
280	285	290	295
tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg			1200
Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro			
300	305	310	
tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac			1248
Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp			
315	320	325	
ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg			1296
Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp			
330	335	340	
tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa			1344
Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln			
345	350	355	
cag tcc aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca			1392
Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala			
360	365	370	375
gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc			1440
Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu			
380	385	390	
gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc			1488
Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala			
395	400	405	
gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg			1536
Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr			
410	415	420	
ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg			1584
Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp			
425	430	435	

235	240	245
Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg		
250	255	260
Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu		
265	270	275
Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn		
280	285	290
Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro		
300	305	310
Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp		
315	320	325
Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp		
330	335	340
Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln		
345	350	355
Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala		
360	365	370
Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu		
380	385	390
Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala		
395	400	405
Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr		
410	415	420
Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp		
425	430	435
Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala		
440	445	450
Glu Val Val Ala Ser Leu Val Pro Ala Ala		
460	465	

<210> 18
<211> 2079
<212> DNA
<213> Unknown

<220>
<221> CDS
<222> (1) ... (2076)

<223> GST:K:trAPAO 2079 nt. Translation starting at nt 1
- 687, gst fusion + polylinker; 688-2076,
K:trAPAO; 2077-2079, stop codon. For bacterial
expression.

<221> misc_feature
<222> (1) ... (687)
<223> gst fusion + polylinker

<221> misc_feature
<222> (688) ... (2076)
<223> K:trAPAO

<221> misc_feature
<222> (688) ... (690)
<223> Extra lysine

<400> 18

atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc	48
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro	
1	5
10	15

act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg	96
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Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu	20	25	30	
tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg				144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu	35	40	45	
ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa				192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys	50	55	60	
tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac				240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn	65	70	75	
atg ttg ggt ggt ttt cca aaa gag cgt gca gag att tca atg ctt gaa				288
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu	85	90	95	
gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt				336
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser	100	105	110	
aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa				384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu	115	120	125	
atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat				432
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn	130	135	140	
ggt gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat				480
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp	145	150	155	
gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta				528
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu	165	170	175	
gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac				576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr	180	185	190	
ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc				624
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala	195	200	205	
acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt				672
Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg	210	215	220	
gga tcc ccg gaa ttc aaa gac aac gtt gcg gac gtg gta gtg gtg ggc				720
Gly Ser Pro Glu Phe Lys Asp Asn Val Ala Asp Val Val Val Val Gly	225	230	235	
gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag gcc gcc ggt				768
Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly	245	250	255	
ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg gga aag act				816
Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr	260	265	270	

ctg	agc	gta	caa	tcg	ggt	ccc	ggc	agg	acg	act	atc	aac	gac	ctc	ggc	864	
Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly		
275						280					285						
gct	gcg	tgg	atc	aat	gac	agc	aac	caa	agc	gaa	gta	tcc	aga	ttg	ttt	912	
Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe		
290						295				300							
gaa	aga	ttt	cat	ttg	gag	ggc	gag	ctc	cag	agg	acg	act	gga	aat	tca	960	
Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser		
305				310				315				320					
atc	cat	caa	gca	caa	gac	ggt	aca	acc	act	aca	gct	cct	tat	ggt	gac	1008	
Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp			
325						330				335							
tcc	ttg	ctg	agc	gag	gag	gtt	gca	agt	gca	ctt	gcg	gaa	ctc	ctc	ccc	1056	
Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro		
340				345			350										
gta	tgg	tct	cag	ctg	atc	gaa	gag	cat	agc	ctt	caa	gac	ctc	aag	gcg	1104	
Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala		
355				360			365										
agc	cct	cag	gcg	aag	cg	ctc	gac	agt	gtg	agc	ttc	g	cac	tac	tgt	1152	
Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys		
370				375			380										
gag	aag	gaa	cta	aac	ttg	cct	gct	gtt	ctc	ggc	gta	gca	aac	cag	atc	1200	
Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile		
385				390			395			400							
aca	cgc	gct	ctc	ggt	gtg	gaa	gcc	cac	gag	atc	agc	atg	ctt	ttt	1248		
Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe		
405						410				415							
ctc	acc	gac	tac	atc	aag	agt	gcc	acc	ggt	ctc	agt	aat	att	ttc	tcg	1296	
Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser		
420						425			430								
gac	aag	aaa	gac	ggc	ggg	cag	tat	atg	cga	tgc	aaa	aca	ggt	atg	cag	1344	
Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln		
435						440			445								
tcg	att	tgc	cat	gcc	atg	tca	aag	gaa	ctt	gtt	cca	ggc	tca	gtg	cac	1392	
Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His		
450						455			460								
ctc	aac	acc	ccc	gtc	gct	gaa	att	gag	cag	tcg	gca	tcc	ggc	tgt	aca	1440	
Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr		
465						470			475			480					
gta	cga	tcg	gcc	tcg	ggc	gcc	gtg	ttc	cga	agc	aaa	aag	gtg	gtg	gtt	1488	
Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val		
485						490			495								
tcg	tta	ccg	aca	acc	ttg	tat	ccc	acc	ttg	aca	ttt	tca	cca	cct	ctt	1536	
Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu		
500						505					510						
ccc	gcc	gag	aag	caa	gca	ttg	g	cg	gaa	aat	tct	atc	ctg	ggc	tac	tat	1584

Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr			
515	520	525	
agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc gaa caa ggc			1632
Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly			
530	535	540	
ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca ttt gcc aga			1680
Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg			
545	550	555	560
gat acc agc atc gac gtc gat cga caa tgg tcc att acc tgt ttc atg			1728
Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met			
565	570	575	
gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag cag gta cga			1776
Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg			
580	585	590	
caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag aac gcc ggg			1824
Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly			
595	600	605	
gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag tgg tcg aag			1872
Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys			
610	615	620	
cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg ctg aac gat			1920
Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp			
625	630	635	640
ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag agt gtt cat			1968
Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His			
645	650	655	
ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat atg gaa ggg			2016
Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly			
660	665	670	
gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg gct agc ctg			2064
Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu			
675	680	685	
gtg cca gca gca tag			2079
Val Pro Ala Ala			
690			
<210> 19			
<211> 692			
<212> PRT			
<213> Unknown			
<220>			
<223> GST:K:trAPAO; GST + linker, aa 1-229; K:trAPAO, aa			
230-692			
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Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro			
1	5	10	15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu			
20	25	30	

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Glu Phe Lys Asp Asn Val Ala Asp Val Val Val Val Gly
 225 230 235 240
 Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly
 245 250 255
 Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr
 260 265 270
 Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly
 275 280 285
 Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe
 290 295 300
 Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser
 305 310 315 320
 Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp
 325 330 335
 Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro
 340 345 350
 Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala
 355 360 365
 Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys
 370 375 380
 Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile
 385 390 395 400
 Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe
 405 410 415
 Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser
 420 425 430
 Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln
 435 440 445
 Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His
 450 455 460
 Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr
 465 470 475 480
 Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val
 485 490 495
 Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu
 500 505 510
 Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr
 515 520 525

Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly
 530 535 540
 Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg
 545 550 555 560
 Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met
 565 570 575
 Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg
 580 585 590
 Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly
 595 600 605
 Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys
 610 615 620
 Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp
 625 630 635 640
 Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His
 645 650 655
 Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly
 660 665 670
 Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu
 675 680 685
 Val Pro Ala Ala
 690

<210> 20
 <211> 1464
 <212> DNA
 <213> Unknown

<220>
 <221> sig_peptide
 <222> (1)...(72)
 <223> Barley Alpha Amylase signal sequence.

<221> misc_feature
 <222> (73)...(1464)
 <223> K:trAPAOcDNA

<221> CDS
 <222> (1)...(1461)

<223> Nucleotide sequence of K:trAPAO translational
 fusion with barley alpha amylase signal sequence,
 for expression and secretion of the mature trAPAO
 in maize. Nucleotides 1-72, barley alpha amylase
 signal sequence, nucleotides 73-75, added lysine
 residue; nucleotides 76 -1464 , trAPAO cDNA.

<221> misc_feature
 <222> (73)...(75)
 <223> Added lysine residue

<400> 20

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 Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly
 -20 -15 -10

48

ctc tcc gcc tcc ctc gcc agc ggc aaa gac aac gtt gcg gac gtg gta
 Leu Ser Ala Ser Leu Ala Ser Gly Lys Asp Asn Val Ala Asp Val Val
 -5 1 5

96

gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag
 Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln

144

10	15	20	
gcc gcc ggt ctg tcc tgc ctc gtt gag gcg atg gat cgt gta ggg Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly 25 30 35 40			192
gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn 45 50 55			240
gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser 60 65 70			288
aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr 75 80 85			336
gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct cct Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro 90 95 100			384
tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu 105 110 115 120			432
ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp 125 130 135			480
ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala 140 145 150			528
cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala 155 160 165			576
aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser 170 175 180			624
atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn 185 190 195 200			672
att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr 205 210 215			720
ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly 220 225 230			768
tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc Ser Val His Leu Asn Thr Pro Val Ala Glu Glu Gln Ser Ala Ser 235 240 245			816
ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys 250 255 260			864

gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser 265 270 275 280	912
cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu 285 290 295	960
ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg 300 305 310	1008
gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser 315 320 325	1056
ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att acc Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr 330 335 340	1104
tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys 345 350 355 360	1152
cag gta cga caa aag tct gtc tgg gac caa ctc ccg gca gcc tac gag Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu 365 370 375	1200
aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu 380 385 390	1248
tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly 395 400 405	1296
ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys 410 415 420	1344
agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr 425 430 435 440	1392
atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val 445 450 455	1440
gct agc ctg gtg cca gca gca tag Ala Ser Leu Val Pro Ala Ala 460	1464

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<211> 487
<212> PRT
<213> Unknown

<220>
<221> SIGNAL
<222> (1)...(24)

<223> K:trAPAO translational fusion with barley alpha amylase signal sequence, for expression and secretion of the mature trAPAO in maize.

<400> 21

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Leu	Ser	Ala	Ser	Leu	Ala	Ser	Gly	Lys	Asp	Asn	Val	Ala	Asp	Val	Val
					-5			1						5	
Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln
					10			15		20					
Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val	Gly
					25			30		35					40
Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn
					45			50			55				
Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser
					60			65					70		
Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr
					75			80			85				
Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro
					90			95			100				
Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu
					105			110		115				120	
Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln	Asp
					125			130			135				
Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala
					140			145			150				
His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val	Ala
					155			160			165				
Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	Ser
					170			175			180				
Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn
					185			190		195				200	
Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr
					205			210			215				
Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro	Gly
					220			225			230				
Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser
					235			240			245				
Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys
					250			255			260				
Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser
					265			270		275				280	
Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu
					285			290			295				
Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg
					300			305			310				
Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser
					315			320			325				
Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr
					330			335			340				
Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys
					345			350		355				360	
Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu
					365			370			375				
Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu
					380			385			390				
Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly
					395			400			405				
Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys
					410			415			420				
Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr

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445	450		455
Ala Ser Leu Val Pro Ala Ala			
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Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro			
1	5	10	15
gca ggg tat tct cac gtc ggc gta ggc cca gac gga ggg agg tat gtg			96
Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val			
20	25	30	
aca ata gct gga cag att gga caa gac gct tcg ggc gtg aca gac cct			144
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro			
35	40	45	
gcc tac gag aaa cag gtt gcc caa gca ttc gcc aat ctg cga gct tgc			192
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys			
50	55	60	
ctt gct gca gtt gga gcc act tca aac gac gtc acc aag ctc aat tac			240
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr			
65	70	75	80
tac atc gtc gac tac gcc ccg agc aaa ctc acc gca att gga gat ggg			288
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly			
85	90	95	
ctg aag gct acc ttt gcc ctt gac agg ctc cct tgc acg ctg gtg			336
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val			
100	105	110	
cca gtg tcg gcc ttg tct tca cct gaa tac ctc ttt gag gtt gat gcc			384
Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala			
115	120	125	
acg gcg ctg gtg ccg gga cac acg acc cca gac aac gtt gcg gac gtg			432
Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val			
130	135	140	
gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc			480
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val			
145	150	155	160
cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag ggc atg gat cgt gta			528
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val			
165	170	175	
ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc			576
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile			

180	185	190	
aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val 195 200 205			624
tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr 210 215 220			672
act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala 225 230 235 240			720
cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala 245 250 255			768
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln 260 265 270			816
gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe 275 280 285			864
gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val 290 295 300			912
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile 305 310 315 320			960
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser 325 330 335			1008
aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys 340 345 350			1056
aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro 355 360 365			1104
ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala 370 375 380			1152
tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys 385 390 395 400			1200
aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe 405 410 415			1248
tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile 420 425 430			1296

ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp 435 440 445	1344
cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile 450 455 460	1392
tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile 465 470 475 480	1440
acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser 485 490 495	1488
aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr 500 505 510	1536
gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile 515 520 525	1584
gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat Glu Trp Ser Lys Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr 530 535 540	1632
ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe 545 550 555 560	1680
aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly 565 570 575	1728
tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val 580 585 590	1776
gtg gct agc ctg gtg cca gca gca tag Val Ala Ser Leu Val Pro Ala Ala 595 600	1803
<p><210> 23 <211> 600 <212> PRT <213> <i>Exophiala spinifera</i></p> <p><400> 23</p> <p>Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro 1 5 10 15 Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val 20 25 30 Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro 35 40 45 Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys 50 55 60 Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr 65 70 75 80 Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly</p>	

85	90	95
Leu Lys Ala Thr Phe Ala Leu Asp Arg	Leu Pro Pro Cys	Thr Leu Val
100	105	110
Pro Val Ser Ala Leu Ser Ser Pro	Glu Tyr Leu Phe Glu Val	Asp Ala
115	120	125
Thr Ala Leu Val Pro Gly His	Thr Thr Pro Asp Asn Val	Ala Asp Val
130	135	140
Val Val Val Gly Ala Gly	Leu Ser Gly Leu Glu Thr Ala Arg	Lys Val
145	150	155
Gln Ala Ala Gly	Leu Ser Cys Leu Val	Leu Glu Ala Met Asp Arg Val
165	170	175
Gly Gly Lys Thr Leu Ser Val Gln	Ser Gly Pro Gly Arg	Thr Thr Ile
180	185	190
Asn Asp Leu Gly Ala Ala Trp	Ile Asn Asp Ser Asn Gln	Ser Glu Val
195	200	205
Ser Arg Leu Phe Glu Arg	Phe His Leu Glu Gly	Glu Leu Gln Arg Thr
210	215	220
Thr Gly Asn Ser Ile His	Gln Ala Gln Asp	Gly Thr Thr Thr Ala
225	230	235
Pro Tyr Gly Asp Ser	Leu Leu Ser Glu Glu Val	Ala Ser Ala Leu Ala
245	250	255
Glu Leu Leu Pro Val Trp Ser	Gln Leu Ile Glu Glu His	Ser Leu Gln
260	265	270
Asp Leu Lys Ala Ser Pro Gln	Ala Lys Arg Leu Asp	Ser Val Ser Phe
275	280	285
Ala His Tyr Cys Glu Lys	Glu Leu Asn Leu Pro	Ala Val Leu Gly Val
290	295	300
Ala Asn Gln Ile Thr Arg	Ala Leu Leu Gly Val	Glu Ala His Glu Ile
305	310	315
Ser Met Leu Phe Leu Thr Asp Tyr	Ile Lys Ser Ala Thr Gly	Leu Ser
325	330	335
Asn Ile Phe Ser Asp Lys	Lys Asp Gly Gly	Gln Tyr Met Arg Cys Lys
340	345	350
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Gly Ser Val His Leu Asn Thr	Pro Val Ala Glu	Ile Glu Gln Ser Ala
370	375	380
Ser Gly Cys Thr Val Arg	Ser Ala Ser Gly	Ala Val Phe Arg Ser Lys
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Lys Val Val Val Ser	Leu Pro Thr Thr	Leu Tyr Pro Thr Leu Thr Phe
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Ser Phe Ala Arg Asp	Thr Ser Ile Asp Val	Asp Arg Gln Trp Ser Ile
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Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu	
90 95 100	
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Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu	
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Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala	
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Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu	
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Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala	
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Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala	
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Pro	Ala	Cys
46	Pro	Gln
60	65	70
Arg	Glu	Ile
Thr	Met	Ala
75	Trp	Phe
Asn	Asn	Thr
76	Pro	Pro
Pro	Ser	Ala
80	85	
Glu	Ser	Gly
Asp	Cys	
90	Leu	Asn
95	Leu	Asn
Ile	Tyr	Ile
100	Val	Pro
105	110	Gly
115	120	Gly
Tyr	Gly	
Trp	Asn	Ser
Phe	His	Leu
125	Tyr	Tyr
Asp	Gly	Ala
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Asn	Gln	Asp
140	Val	Ile
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160	Ala	Thr
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190	Val	Val
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205	Asp	Val
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Pro	Pro	His
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275	Ile	Arg
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365	Ala	Thr
370	Ala	Glu
375	Ile	Val
Val	Ala	Gln
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385	Ser	Arg
390	Gly	Asn
Tyr	Asn	Arg
395	Ala	Thr
400	Phe	Glu
405	Asn	Leu
Tyr	His	Gly
410	Ser	Glu
415	Ser	Val
420	Gly	Gly
Ser	Ala	Met
425	Thr	Val
430	Ala	Phe
435	Gln	Ala
Trp	Ala	Lys
445	Ala	Asn
450	Phe	Pro
455	Asn	Gly
Val	Pro	Trp
460	Asn	Lys
465	Val	Trp
470	Ala	Lys
Asp	Val	Ala
475	Ser	Thr
480	Pro	Asn
485	Ala	Asn
Tyr	Tyr	Glu
490	Thr	Leu
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515	Ser	Gly
520	Lys	Asp
Val	Val	Asn
525	Val	Val
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535	Leu	Asp
Gln	Ala	Ala
	Gly	Arg
	Leu	Val
	Ser	Asp
	Cys	Arg
	Leu	Val
	Glu	Val
	Ala	Val

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	Ala	Trp
		Ile
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		Gln
		Ser
		Gly
		Pro
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		Arg
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		Thr
		Ile
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		Ile
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		Asn
		Gln
		Ser
		Glu
		Val
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		Glu
		Gly
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		Thr
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		Ala
		Gln
		Asp
		Gly
		Thr
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		Ala
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		Leu
		Ser
		Glu
		Glu
		Val
		Ala
		Ser
		Ala
		Leu
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	Pro	Val
		Trp
		Ser
		Gln
		Leu
		Ile
		Glu
		Glu
		His
		Ser
		Leu
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	Ala	Ser
		Pro
		Gln
		Ala
		Lys
		Arg
		Leu
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		Ser
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		Lys
		Glu
		Leu
		Asn
		Leu
		Pro
		Ala
		Val
		Leu
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		Thr
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		Ala
		Leu
		Gly
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		Ala
		His
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	Thr	Asp
		Tyr
		Ile
		Lys
		Ser
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		Thr
		Gly
		Leu
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		Lys
		Asp
		Gly
		Gly
		Gln
		Tyr
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		Cys
		His
		Ala
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		Thr
		Pro
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		Ser
		Ala
		Ser
		Gly
		Ala
		Val
		Phe
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		Leu
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		Glu
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		Gln
		Ala
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		Ile
		Val
		Phe
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	Gly	Phe
	Ser	Gly
		Val
		Leu
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	Arg	Asp
		Thr
		Ser
		Ile
845	850	855
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		Asp
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		Glu
		Pro
		Ala
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	Lys	Gln
		Gln
		Tyr
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		Ile
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		Gly
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		His
		Phe
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Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser
      75                 80                 85

ggc gct aaa ccc ggc cag tac ccc gtc atg gtc tgg gtc tac ggc ggc 384
Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly
      90                 95                 100

ggc ttc gcc ggc ggc acg gcc gcc atg ccc tac tac gac ggc gag gcg 432
Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala

```

105	110	115	120	
ctt gcg cga cag ggc gtc gtc gtg acg ttt aac tat cgg acg aac				480
Leu Ala Arg Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn				
125 130 135				
atc ctg ggc ttt ttc gcc cat cct ggt ctc tcg cgc gag agc ccc acc				528
Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr				
140 145 150				
gga act tcg ggc aac tac ggc cta ctc gac att ctc gcc gct ctt cgg				576
Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg				
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Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val				
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Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu				
185 190 195 200				
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Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser				
205 210 215				
cca ggg ctg acg cga ccg ctc gcg acg ctc gcc gac agc gcc gcc tcg				768
Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser				
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ggc gag cgc ctc gac gcc gat ctt tcg cga ctg cgc tcg acc gac cca				816
Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro				
235 240 245				
gcc acc ctg atg gcg cgc gcc gac gcg gcc cgc ccg gca tcg cgg gac				864
Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp				
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ctg cgc agg ccg cgt ccg acc gga ccg atc gtc gat ggc cat gtg ctg				912
Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu				
265 270 275 280				
ccg cag acc gac agc gcg gcg atc gcg gcg ggg cag ctg gcg ccg gtt				960
Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val				
285 290 295				
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Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly				
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Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala				
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Gln Phe Gly Asp Gln Ala Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp				
330 335 340				
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Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn				
345 350 355 360				

cag ttc aat cgg ggg gtc tcg gcc ttc tcg gaa gcg ctt gtg cgc cag Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln 365	370	375	1200	
ggc gcg ccc gtg tgg cgt tat cag ttc aac ggt aat acc gag ggt gga Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly 380	385	390	1248	
aga gcg ccc gct acc cac gga gcc gaa att ccc tac gtt ttc ggg gtg Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val 395	400	405	1296	
ttc aag ctc gac gag ttg ggt ctg ttc gat tgg ccg ccc gag ggg ccc Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro 410	415	420	1344	
acg ccc gcc gac cgt gcg ctg ggc caa ctg atg tcc tcc gcc tgg gtc Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val 425	430	435	440	1392
cgg ttc gcc aag aat ggc gac ccc gcc ggg gac gcc ctt acc tgg cct Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro 445	450	455	1440	
gcc tat tct acg ggc aag tcg acc atg aca ttc ggt ccc gag ggc cgc Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg 460	465	470	1488	
gcf gcf gtg gtg tcg ccc gga cct tcc atc ccc cct tgc gcf gat ggc Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly 475	480	485	1536	
gcc aag gcf ggg ggc gga ggc agc ggc gga ggc agc ggc gga ggc agc Ala Lys Ala Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Ser 490	495	500	1584	
aaa gac aac gtt gcf gac gtg gta gtg gtg ggc gct ggc ttg agc ggt Lys Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly 505	510	515	520	1632
ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val 525	530	535	1680	
ctt gag gcf atg gat cgt gta ggg gga aag act ctg agc gta caa tcg Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser 540	545	550	1728	
ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcf tgg atc aat Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn 555	560	565	1776	
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu 570	575	580	1824	
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln 585	590	595	600	1872
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630			
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys	635	640	2016
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cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn	650	655	2064
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675			
680			
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695			
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly	700	705	2208
710			
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala	715	720	2256
725			
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val	730	735	2304
740			
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser	745	750	2352
755			
760			
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr	765	770	2400
775			
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln	780	785	2448
790			
795			
800			
805			
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe	805		2496
810			
815			
820			
caa tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp	825	830	2592
835			
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gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly	845	850	2640
855			

cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg 2688
 Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
 860 865 870

gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag 2736
 Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
 875 880 885

ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa 2784
 Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
 890 895 900

gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt 2832
 Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
 905 910 915 920

tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag 2880
 Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
 925 930 935

acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt 2928
 Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
 940 945 950

caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca 2973
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tag 2976

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 Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg
 10 15 20
 Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro
 25 30 35 40
 Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe
 45 50 55
 Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala
 60 65 70
 Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser
 75 80 85
 Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly
 90 95 100
 Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala
 105 110 115 120
 Leu Ala Arg Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn
 125 130 135
 Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr
 140 145 150

Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg
 155 160 165
 Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val
 170 175 180
 Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu
 185 190 195 200
 Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser
 205 210 215
 Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser
 220 225 230
 Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro
 235 240 245
 Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp
 250 255 260
 Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu
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 Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val
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 Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly
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 Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala
 315 320 325
 Gln Phe Gly Asp Gln Ala Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp
 330 335 340
 Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn
 345 350 355 360
 Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln
 365 370 375
 Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly
 380 385 390
 Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val
 395 400 405
 Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro
 410 415 420
 Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val
 425 430 435 440
 Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro
 445 450 455
 Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg
 460 465 470
 Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly
 475 480 485
 Ala Lys Ala Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser
 490 495 500
 Lys Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly
 505 510 515 520
 Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
 525 530 535
 Leu Glu Ala Met Asp Arg Val Gly Lys Thr Leu Ser Val Gln Ser
 540 545 550
 Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
 555 560 565
 Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
 570 575 580
 Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
 585 590 595 600
 Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
 605 610 615
 Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
 620 625 630
 Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
 635 640 645

Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
 650 655 660
 Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
 665 670 675 680
 Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
 685 690 695
 Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
 700 705 710
 Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala
 715 720 725
 Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
 730 735 740
 Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
 745 750 755 760
 Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
 765 770 775
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 780 785 790
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 795 800 805
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 810 815 820
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 825 830 835 840
 Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
 845 850 855
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 860 865 870
 Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
 875 880 885
 Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
 890 895 900
 Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
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 Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
 925 930 935
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<212> DNA

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 2227-3615, K:trAPAO, extra lysine; 3616-3618, stop
 codon. For bacterial expression.

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<223> gast + polylinker

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1	5								10					15		

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 Thr Arg Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30

tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
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 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
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 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80

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 115 120 125

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 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
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 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
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 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
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gac tgc ctg aac ctc aac atc tac gtc cca gga act gag aac aca aac Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu Asn Thr Asn 325 330 335	1008
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gct gcc cct cag ctt cca ata aca cag cga aat ctg ggg ttc cta gac Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly Phe Leu Asp 385 390 395 400	1200
caa agg ttt gct ttg gat tgg gta cag cgg aac atc gca gcc ttt ggc Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala Ala Phe Gly 405 410 415	1248
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435	440	445	
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gat ttg tcc gaa cct tgg aac acc act gtt caa gct ctc aac tgt acc Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu Asn Cys Thr 465	470	475	1440
acc agt atc gac atc ttg agt tgt atg aga aga gtc gat ctc gcc act Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp Leu Ala Thr 485	490	495	1488
ctg atg aac acg atc gag caa ctc gga ctt ggg ttt gag tac acg ttg Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu Tyr Thr Leu 500	505	510	1536
gac aac gta acg gct gtg tac cgt tct gaa acg gct cgc acg act ggt Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg Thr Thr Gly 515	520	525	1584
gac att gct cgt gta cct gtt ctc gtc ggg acg gtg gcc aac gac gga Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala Asn Asp Gly 530	535	540	1632
ctt ctc ttt gtc ctc ggg gag aat gac acc caa gca tat ctc gag gag Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr Leu Glu Glu 545	550	555	1680
gca atc ccg aat cag ccc gac ctt tac cag act ctc ctt gga gca tat Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu Gly Ala Tyr 565	570	575	1728
ccc att gga tcc cca ggg atc gga tcg cct caa gat cag att gcc gcc Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln Ile Ala Ala 580	585	590	1776
att gag acc gag gta aga ttc cag tgt cct tct gcc atc gtg gct cag Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile Val Ala Gln 595	600	605	1824
gac tcc cgg aat cgg ggt atc cct tct tgg cgc tac tac tac aat gcg Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr Tyr Asn Ala 610	615	620	1872
acc ttt gag aat ctg gag ctt ttc cct ggg tcc gaa gtg tac cac agc Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val Tyr His Ser 625	630	635	1920
tct gaa gtc ggg atg gtg ttt ggc acg tat cct gtc gca agt gcg acc Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala Ser Ala Thr 645	650	655	1968
gcc ttg gag gcc cag acg agc aaa tac atg cag ggt gcc tgg gcg gcc Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala Trp Ala Ala 660	665	670	2016
ttt gcc aaa aac ccc atg aat ggg cct ggg tgg aaa caa gtg ccg aat Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln Val Pro Asn 675	680	685	2064

gtc gcg gcg ctt ggc tca cca ggc aaa gcc atc cag gtt gac gtc tct Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val Asp Val Ser 690 695 700	2112
cca gcg aca ata gac caa cga tgt gcc ttg tac acg cgt tat tat act Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg Tyr Tyr Thr 705 710 715 720	2160
gag ttg ggc aca atc gcg ccg agg aca ttt ggc gga ggc agc ggc gga Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Ser Gly Gly 725 730 735	2208
ggc agc ggc gga ggc agc aaa gac aac gtt gcg gac gtg gta gtg gtg Gly Ser Gly Gly Ser Lys Asp Asn Val Ala Asp Val Val Val Val 740 745 750	2256
ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag gcc gcc Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala 755 760 765	2304
ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg gga aag Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys 770 775 780	2352
act ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac gac ctc Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu 785 790 795 800	2400
ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc aga ttg Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu 805 810 815	2448
ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act gga aat Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn 820 825 830	2496
tca atc cat caa gca caa gac ggt aca acc act aca gct cct tat ggt Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr Gly 835 840 845	2544
gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa ctc ctc Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu 850 855 860	2592
ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac ctc aag Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys 865 870 875 880	2640
gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg cac tac Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr 885 890 895	2688
tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca aac cag Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln 900 905 910	2736
atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc atg ctt Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu 915 920 925	2784
ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat att ttc Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe	2832

930	935	940	
tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca ggt atg			2880
Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met			
945	950	955	960
cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc tca gtg			2928
Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val			
965	970	975	
cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc ggc tgt			2976
His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys			
980	985	990	
aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag gtg gtg			3024
Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val			
995	1000	1005	
gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca cca cct			3072
Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro			
1010	1015	1020	
ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg ggc tac			3120
Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr			
1025	1030	1035	1040
tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc gaa caa			3168
Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln			
1045	1050	1055	
ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca ttt gcc			3216
Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala			
1060	1065	1070	
aga gat acc agc atc gac gtc gat cga caa tgg tcc att acc tgt ttc			3264
Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe			
1075	1080	1085	
atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag cag gta			3312
Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val			
1090	1095	1100	
cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag aac gcc			3360
Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala			
1105	1110	1115	1120
ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag tgg tcg			3408
Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser			
1125	1130	1135	
aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg ctg aac			3456
Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn			
1140	1145	1150	
gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag agt gtt			3504
Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val			
1155	1160	1165	
cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat atg gaa			3552
His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu			
1170	1175	1180	

ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg gct agc 3600
 Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser
 1185 1190 1195 1200

ctg gtg cca gca gca tag 3618
 Leu Val Pro Ala Ala
 1205

<210> 29
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 <212> PRT
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<400> 29

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 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala 195 200 205
 Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg 210 215 220
 Gly Ser Pro Glu Phe Ala Pro Thr Val Lys Ile Asp Ala Gly Met Val 225 230 235 240
 Val Gly Thr Thr Thr Val Pro Gly Thr Thr Ala Thr Val Ser Glu 245 250 255
 Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe Ala Pro Pro 260 265 270
 Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr Ala Tyr Gly 275 280 285
 Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu Arg Glu Ile 290 295 300
 Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly Glu Ser Glu 305 310 315 320
 Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu Asn Thr Asn 325 330 335
 Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu Tyr Gly Trp 340 345 350
 Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala Asn Gln Asp 355 360 365
 Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu Gly Phe Pro

370	375	380
Ala	Ala	Pro
385	390	395
Gln	Arg	Phe
Arg	Phe	Ala
Asp	Trp	Leu
Trp	Val	Gln
Val	Arg	Arg
Gly	Asn	Ile
Asn	Ile	Ala
Ile	Ala	Phe
405	410	415
Gly	Asp	Pro
Asp	Arg	Lys
Lys	Val	Thr
Val	Ile	Phe
Phe	Gly	Gln
Gln	Ser	Ala
Ser	Gly	Gly
Gly	Arg	Arg
Arg	420	425
Ser	Val	Asp
Asp	Val	Leu
Leu	Leu	Thr
Thr	Ser	Met
Met	Pro	His
His	Asn	Pro
Pro	Pro	Phe
Phe	Arg	Arg
Arg	435	440
Ser	Val	Asp
Asp	Val	Leu
Leu	Leu	Thr
Thr	Ser	Met
Met	Pro	His
His	Asn	Pro
Pro	Pro	Phe
Phe	Arg	Arg
Arg	445	450
Ala	Ala	Ile
Ile	Met	Glu
Glu	Ser	Gly
Gly	Val	Ala
Ala	Asn	Tyr
Tyr	Asn	Phe
Phe	Pro	Lys
Lys	Gly	
450	455	460
Asp	Leu	Ser
Ser	Glu	Pro
Pro	Trp	Asn
Trp	Thr	Thr
Thr	Val	Gln
Gln	Ala	Leu
Leu	Asn	Cys
Cys	Thr	
465	470	475
Thr	Ser	Ile
Ile	Asp	Ile
Asp	Leu	Ser
Ser	Cys	Met
Met	Arg	Arg
Arg	Val	Asp
Asp	Leu	Ala
Ala	Thr	
485	490	495
Leu	Met	Asn
Asn	Thr	Ile
Ile	Glu	Gln
Gln	Leu	Gly
Gly	Leu	Phe
Phe	Glu	Tyr
Tyr	Thr	Leu
Leu	500	505
Asp	Asn	Val
Asn	Thr	Ala
Thr	Ala	Val
Val	Tyr	Arg
Arg	Ser	Glu
Glu	Thr	Ala
Ala	Arg	Thr
Thr	Thr	Gly
Gly	515	520
Asp	Ile	Ala
Ala	Arg	Val
Val	Pro	Val
Leu	Leu	Gly
Gly	Thr	Val
Val	Ala	Asn
Asn	Asp	Gly
Gly	530	535
Leu	Leu	Phe
Phe	Val	Leu
Leu	Gly	Glu
Glu	Asn	Asp
Asp	Thr	Gln
Gln	Ala	Tyr
Tyr	Leu	Glu
Glu	545	550
Ala	Ile	Pro
Pro	Gln	Asn
Asn	Pro	Asp
Asp	Leu	Tyr
Tyr	Gln	Thr
Thr	Leu	Leu
Leu	Gly	Tyr
Tyr	Ala	
555	560	565
Asp	Ile	Arg
Arg	Val	Pro
Pro	Val	Leu
Leu	Val	Gly
Gly	Thr	Val
Val	Ala	Asp
Asp	575	580
Ile	Gly	Ser
Ser	Pro	Gly
Gly	Ile	Gly
Gly	Ser	Pro
Pro	Gln	Asp
Asp	Ile	Ala
Ala	585	590
Ile	Glu	Thr
Thr	Glu	Val
Val	Arg	Phe
Phe	Gln	Cys
Cys	Pro	Ser
Ser	Ala	Ile
Ile	595	600
Val	Glu	Asn
Asn	Arg	Arg
Arg	Gly	Ile
Ile	Pro	Ser
Ser	Trp	Arg
Arg	Tyr	Tyr
Tyr	Tyr	Asn
Asn	Ala	Ala
Ala	610	615
Thr	Phe	Glu
Glu	Asn	Leu
Leu	Glu	Leu
Leu	Phe	Pro
Pro	Gly	Ser
Ser	Glu	Val
Val	Tyr	Tyr
Tyr	His	Ser
Ser	625	630
Asn	Asn	Leu
Leu	Glu	Glu
Glu	Leu	Leu
Leu	Asn	Asp
Asp	635	640
Thr	Glu	Val
Val	Asn	Asp
Asp	645	650
Ser	Glu	Val
Val	Gly	Met
Met	Val	Phe
Phe	Gly	Thr
Thr	Tyr	Tyr
Tyr	Pro	Val
Val	Ala	Ser
Ser	655	660
Ala	Ile	Pro
Pro	Asn	Gln
Gln	Pro	Asp
Asp	Leu	Tyr
Tyr	Gln	Thr
Thr	Leu	Leu
Leu	Gly	Tyr
Tyr	Ala	
665	670	675
Phe	Ala	Lys
Lys	Asn	Pro
Pro	Met	Asn
Asn	Gly	Pro
Pro	Gly	Trp
Trp	Lys	Gln
Gln	Val	Pro
Pro	Asn	Asn
Asn	675	680
Val	Ala	Ala
Ala	685	690
Leu	Gly	Ser
Ser	Pro	Gly
Gly	Lys	Asp
Asp	Ala	Ile
Ile	695	700
Pro	Ala	Thr
Thr	Ile	Asp
Asp	Gln	Arg
Arg	Cys	Ala
Ala	Leu	Tyr
Tyr	Thr	Arg
Arg	Tyr	Tyr
Tyr	Thr	Thr
710	715	720
Glu	Leu	Gly
Gly	Thr	Ile
Ile	Ala	Pro
Pro	Arg	Thr
Thr	Phe	Gly
Gly	Gly	Gly
Gly	725	730
Gly	Ser	Gly
Gly	Gly	Ser
Ser	Lys	Asp
Asp	Asn	Val
Val	Ala	Asp
Asp	735	740
Val	Val	Val
Val	Val	Val
Val	745	750
Gly	Ala	Gly
Gly	Leu	Ser
Ser	Gly	Leu
Leu	Glu	Thr
Thr	Ala	Arg
Arg	Lys	Val
Val	Gln	Ala
Ala	755	760
Gly	Leu	Ser
Ser	Cys	Leu
Leu	Val	Leu
Leu	Glu	Ala
Ala	Met	Asp
Asp	Arg	Val
Val	Gly	Gly
Gly	Lys	765
770	775	780
Thr	Leu	Ser
Ser	Val	Gln
Gln	Ser	Gly
Gly	Pro	Arg
Arg	Thr	Thr
Thr	Ile	Asn
Asn	Asp	Leu
785	790	795
Gly	Ala	Ala
Ala	795	800
Trp	Ile	Asn
Asp	Asn	Asp
Asp	Asn	Asn
Asn	Gln	Ser
Ser	Glu	Val
Val	Ala	Ser
Ser	810	815
Phe	Glu	Arg
Glu	Arg	Phe
Phe	His	Leu
His	Leu	Glu
Gly	Gly	Glu
Gly	Glu	Glu
Glu	Leu	Gly
Gly	Leu	Gly
Gly	Arg	Thr
Arg	Thr	Thr
Thr	Ile	Asn
Asn	Asp	Leu
820	825	830
Ser	Ile	His
His	Gln	Ala
Ala	Gln	Asp
Asp	Gly	Thr
Thr	Thr	Thr
Thr	Thr	Ala
Ala	Pro	Tyr
Tyr	Gly	Gly
Gly	835	840
Asp	Ser	Leu
Leu	Leu	Ser
Ser	Glu	Glu
Glu	Val	Ala
Ala	Ser	Ala
Ala	850	855
Glu	Leu	Glu
Glu	Leu	Leu
Leu	Leu	Lys
Leu	860	
Pro	Val	Trp
Trp	Ser	Gln
Gln	Leu	Ile
Ile	Glu	Glu
Glu	Glu	His
His	Ser	Leu
Leu	Gln	Asp
Asp	Leu	Lys

865	870	875	880
Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr			
885	890	895	
Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln			
900	905	910	
Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu			
915	920	925	
Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe			
930	935	940	
Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met			
945	950	955	960
Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val			
965	970	975	
His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys			
980	985	990	
Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val			
995	1000	1005	
Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro			
1010	1015	1020	
Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr			
1025	1030	1035	1040
Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln			
1045	1050	1055	
Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala			
1060	1065	1070	
Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe			
1075	1080	1085	
Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val			
1090	1095	1100	
Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala			
1105	1110	1115	1120
Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser			
1125	1130	1135	
Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn			
1140	1145	1150	
Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val			
1155	1160	1165	
His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu			
1170	1175	1180	
Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser			
1185	1190	1195	1200
Leu Val Pro Ala Ala			
1205			

<210> 30

<211> 3591

<212> DNA

<213> Unknown

<220>

<223> Open reading frame of BEST1:K:trAPAO fusion for bacterial expression vector pGEX-4T-1 or similar vector.

gst:BEST1:sp:K:trAPAO fusion, 3591 nt. 1-687 gst + polylinker, 688-2163, BEST1 mature; 2164-2199, spacer, 2200-3588, K:trAPAO

<221> misc_feature

<222> (1)...(687)

<223> gst + polylinker

<221> mat_peptide

<222> (688) ... (2163)

<223> BEST1 mature

<221> misc_feature

<222> (2164) ... (2199)

<223> spacer sequence

<221> misc_feature

<222> (2200) ... (3588)

<223> K:trAPAO

<221> CDS

<222> (1) ... (3588)

<221> misc_feature

<222> (2200) ... (2202)

<223> Extra lysine

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act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg	96
Thr Arg Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu	
20 25 30	

tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg	144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu	
35 40 45	

ggg ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa	192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys	
50 55 60	

tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac	240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn	
65 70 75 80	

atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa	288
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu	
85 90 95	

gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt	336
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser	
100 105 110	

aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa	384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu	
115 120 125	

atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat	432
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn	
130 135 140	

ggg gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat	480
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp	
145 150 155 160	

gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta	528
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu	
165 170 175	

gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac		576	
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr			
180	185	190	
ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc		624	
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala			
195	200	205	
acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt		672	
Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg			
210	215	220	
gga tcc ccg gaa ttc acg gat ttt ccg gtc cgc agg acc gat ctg ggc		720	
Gly Ser Pro Glu Phe Thr Asp Phe Pro Val Arg Arg Thr Asp Leu Gly			
225	230	235	240
cag gtt cag gga ctg gcc ggg gac gtg atg agc ttt cgc gga ata ccc		768	
Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg Gly Ile Pro			
245	250	255	
tat gca gcg ccg ccg gtg ggc ggg ctg cgt tgg aag ccg ccc caa cac		816	
Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro Pro Gln His			
260	265	270	
gcc cgg ccc tgg gcg ggc gtt cgc ccc gcc acc caa ttt ggc tcc gac		864	
Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe Gly Ser Asp			
275	280	285	
tgc ttc ggc gcg gcc tat ctt cgc aaa ggc agc ctc gcc ccc ggc gtg		912	
Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala Pro Gly Val			
290	295	300	
agc gag gac tgt ctt tac ctc aac gta tgg gcg ccg tca ggc gct aaa		960	
Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser Gly Ala Lys			
305	310	315	320
ccc ggc cag tac ccc gtc atg gtc tgg gtc tac ggc ggc ggc ttc gcc		1008	
Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly Phe Ala			
325	330	335	
ggc ggc acg gcc gcc atg ccc tac tac gac ggc gag gcg ctt gcg cga		1056	
Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala Leu Ala Arg			
340	345	350	
cag ggc gtc gtc gtg acg ttt aac tat cgg acg aac atc ctg ggc		1104	
Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn Ile Leu Gly			
355	360	365	
ttt ttc gcc cat cct ggt ctc tcg cgc gag agc ccc acc gga act tcg		1152	
Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr Gly Thr Ser			
370	375	380	
ggc aac tac ggc cta ctc gac att ctc gcc gct ctt cgg tgg gtg cag		1200	
Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg Trp Val Gln			
385	390	395	400
agc aac gcc cgc gcc ttc gga ggg gac ccc ggc cga gtg acg gtc ttt		1248	
Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val Thr Val Phe			
405	410	415	
ggt gaa tcg gcc gga gcg agc gcg atc gga ctt ctg ctc acc tcg ccg		1296	

Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu Thr Ser Pro			
420	425	430	
ctg agc aag ggt ctc ttc cgt ggc gct atc ctc gaa agt cca ggg ctg			1344
Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser Pro Gly Leu			
435	440	445	
acg cga ccg ctc gcg acg ctc gcc gac agc gcc tcg ggc gag cgc			1392
Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser Gly Glu Arg			
450	455	460	
ctc gac gcc gat ctt tcg cga ctg cgc tcg acc gac cca gcc acc ctg			1440
Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro Ala Thr Leu			
465	470	475	480
atg gcg cgc gcc gac gcg gcc cgc ccg gca tcg cgg gac ctg cgc agg			1488
Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp Leu Arg Arg			
485	490	495	
ccg cgt ccg acc gga ccg atc gtc gat ggc cat gtg ctg ccg cag acc			1536
Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu Pro Gln Thr			
500	505	510	
gac agc gcg gcg atc gcg gcg ggg cag ctg gcg ccg gtt cgg gtc ctg			1584
Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val Arg Val Leu			
515	520	525	
atc gga acc aat gcc gac gaa ggc cgc gcc ttc ctc ggg cgc gcg ccg			1632
Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly Arg Ala Pro			
530	535	540	
atg gag acg cca gcg gac tac caa gcc tat ctg gag gcg cag ttt ggc			1680
Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala Gln Phe Gly			
545	550	555	560
gac caa gcc gcc gtg gcg tgc tat ccc ctc gac ggc cgg gcc			1728
Asp Gln Ala Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp Gly Arg Ala			
565	570	575	
acg ccc aag gaa atg gtc gcg cgc atc ttc ggc gac aat cag ttc aat			1776
Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn Gln Phe Asn			
580	585	590	
cgg ggg gtc tcg gcc ttc tcg gaa ggc ctt gtg cgc cag ggc gcg ccc			1824
Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln Gly Ala Pro			
595	600	605	
gtg tgg cgt tat cag ttc aac ggt aat acc gag ggt gga aga gcg ccg			1872
Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Arg Ala Pro			
610	615	620	
gct acc cac gga gcc gaa att ccc tac gtt ttc ggg gtg ttc aag ctc			1920
Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val Phe Lys Leu			
625	630	635	640
gac gag ttg ggt ctg ttc gat tgg ccg ccc gag ggg ccc acg ccc gcc			1968
Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro Thr Pro Ala			
645	650	655	
gac cgt gcg ctg ggc caa ctg atg tcc tcc gcc tgg gtc cgg ttc gcc			2016
Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val Arg Phe Ala			
660	665	670	

aag aat ggc gac ccc gcc ggg gac gcc ctt acc tgg cct gcc tat tct	2064
Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro Ala Tyr Ser	
675 680 685	
acg ggc aag tcg acc atg aca ttc ggt ccc gag ggc cgc gcg gtc	2112
Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg Ala Ala Val	
690 695 700	
gtg tcg ccc gga cct tcc atc ccc cct tgc gcg gat ggc gcc aag gcg	2160
Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly Ala Lys Ala	
705 710 715 720	
ggg ggc gga ggc agc ggc gga ggc agc ggc gga ggc agc aaa gac aac	2208
Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Lys Asp Asn	
725 730 735	
gtt gcg gac gtg gta gtg gtc gct ggc ttg agc ggt ttg gag acg	2256
Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr	
740 745 750	
gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg	2304
Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala	
755 760 765	
atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt ccc ggc	2352
Met Asp Arg Val Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly	
770 775 780	
agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac agc aac	2400
Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn	
785 790 795 800	
caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag	2448
Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu	
805 810 815	
ctc cag agg acg act gga aat tca atc cat caa gca caa gac ggt aca	2496
Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr	
820 825 830	
acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt gca	2544
Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala	
835 840 845	
agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag	2592
Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu	
850 855 860	
cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg ctc gac	2640
His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp	
865 870 875 880	
agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg cct gct	2688
Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala	
885 890 895	
gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa	2736
Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu	
900 905 910	
gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag agt gcc	2784

Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala			
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acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg cag tat			2832
Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr			
930	935	940	
atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg tca aag			2880
Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys			
945	950	955	960
gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa att			2928
Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile			
965	970	975	
gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg			2976
Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val			
980	985	990	
ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc			3024
Phe Arg Ser Lys Lys Val Val Ser Leu Pro Thr Thr Leu Tyr Pro			
995	1000	1005	
acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg gcg			3072
Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala			
1010	1015	1020	
gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg gac			3120
Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp			
1025	1030	1035	1040
aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc			3168
Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser			
1045	1050	1055	
tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat cga			3216
Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg			
1060	1065	1070	
caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg			3264
Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp			
1075	1080	1085	
tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac caa ctc			3312
Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu			
1090	1095	1100	
cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac			3360
Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn			
1105	1110	1115	1120
gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct ccg			3408
Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro			
1125	1130	1135	
agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc			3456
Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu			
1140	1145	1150	
aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct tta			3504
Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu			
1155	1160	1165	

gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt 3552
 Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly
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1185 . 1190 . 1195

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<211> 1196
<212> PRT
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<400> 31

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				20				25					30		
Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu
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Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys
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Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn
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Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu
					85			90					95		
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser
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Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu
					115		120				125				
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn
					130		135				140				
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp
					145		150				155			160	
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu
					165				170			175			
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr
					180			185				190			
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala
					195			200				205			
Thr	Phe	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg	
					210		215				220				
Gly	Ser	Pro	Glu	Phe	Thr	Asp	Phe	Pro	Val	Arg	Arg	Thr	Asp	Leu	Gly
					225		230				235			240	
Gln	Val	Gln	Gly	Leu	Ala	Gly	Asp	Val	Met	Ser	Phe	Arg	Gly	Ile	Pro
					245			250				255			
Tyr	Ala	Ala	Pro	Pro	Val	Gly	Gly	Leu	Arg	Trp	Lys	Pro	Pro	Gln	His
					260			265				270			
Ala	Arg	Pro	Trp	Ala	Gly	Val	Arg	Pro	Ala	Thr	Gln	Phe	Gly	Ser	Asp
					275		280				285				
Cys	Phe	Gly	Ala	Ala	Tyr	Leu	Arg	Lys	Gly	Ser	Leu	Ala	Pro	Gly	Val
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Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Val	Trp	Ala	Pro	Ser	Gly	Ala	Lys
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Pro	Gly	Gln	Tyr	Pro	Val	Met	Val	Trp	Val	Tyr	Gly	Gly	Phe	Ala	
					325			330				335			
Gly	Gly	Thr	Ala	Ala	Met	Pro	Tyr	Tyr	Asp	Gly	Glu	Ala	Leu	Ala	Arg
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Gln	Gly	Val	Val	Val	Val	Thr	Phe	Asn	Tyr	Arg	Thr	Asn	Ile	Leu	Gly

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Phe	Phe	Ala	His	Pro	Gly	Leu	Ser	Arg	Glu	Ser	Pro	Thr	Gly	Thr	Ser
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Gly	Asn	Tyr	Gly	Leu	Leu	Asp	Ile	Leu	Ala	Ala	Leu	Arg	Trp	Val	Gln
385						390					395				400
Ser	Asn	Ala	Arg	Ala	Phe	Gly	Gly	Asp	Pro	Gly	Arg	Val	Thr	Val	Phe
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Gly	Glu	Ser	Ala	Gly	Ala	Ser	Ala	Ile	Gly	Leu	Leu	Leu	Thr	Ser	Pro
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Leu	Ser	Lys	Gly	Leu	Phe	Arg	Gly	Ala	Ile	Leu	Glu	Ser	Pro	Gly	Leu
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Thr	Arg	Pro	Leu	Ala	Thr	Leu	Ala	Asp	Ser	Ala	Ala	Ser	Gly	Glu	Arg
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Leu	Asp	Ala	Asp	Leu	Ser	Arg	Leu	Arg	Ser	Thr	Asp	Pro	Ala	Thr	Leu
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Met	Ala	Arg	Ala	Asp	Ala	Ala	Arg	Pro	Ala	Ser	Arg	Asp	Leu	Arg	Arg
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Pro	Arg	Pro	Thr	Gly	Pro	Ile	Val	Asp	Gly	His	Val	Leu	Pro	Gln	Thr
											500				510
Asp	Ser	Ala	Ala	Ile	Ala	Ala	Gly	Gln	Leu	Ala	Pro	Val	Arg	Val	Leu
											515				525
Ile	Gly	Thr	Asn	Ala	Asp	Glu	Gly	Arg	Ala	Phe	Leu	Gly	Arg	Ala	Pro
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Met	Glu	Thr	Pro	Ala	Asp	Tyr	Gln	Ala	Tyr	Leu	Glu	Ala	Gln	Phe	Gly
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Asp	Gln	Ala	Ala	Ala	Val	Ala	Ala	Cys	Tyr	Pro	Leu	Asp	Gly	Arg	Ala
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Thr	Pro	Lys	Glu	Met	Val	Ala	Arg	Ile	Phe	Gly	Asp	Asn	Gln	Phe	Asn
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Arg	Gly	Val	Ser	Ala	Phe	Ser	Glu	Ala	Leu	Val	Arg	Gln	Gly	Ala	Pro
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Val	Trp	Arg	Tyr	Gln	Phe	Asn	Gly	Asn	Thr	Glu	Gly	Gly	Arg	Ala	Pro
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Ala	Thr	His	Gly	Ala	Glu	Ile	Pro	Tyr	Val	Phe	Gly	Val	Phe	Lys	Leu
											625				640
Asp	Glu	Leu	Gly	Leu	Phe	Asp	Trp	Pro	Pro	Glu	Gly	Pro	Thr	Pro	Ala
											645				655
Asp	Arg	Ala	Leu	Gly	Gln	Leu	Met	Ser	Ser	Ala	Trp	Val	Arg	Phe	Ala
											660				670
Lys	Asn	Gly	Asp	Pro	Ala	Gly	Asp	Ala	Leu	Thr	Trp	Pro	Ala	Tyr	Ser
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Thr	Gly	Lys	Ser	Thr	Met	Thr	Phe	Gly	Pro	Glu	Gly	Arg	Ala	Ala	Val
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Val	Ser	Pro	Gly	Pro	Ser	Ile	Pro	Pro	Cys	Ala	Asp	Gly	Ala	Lys	Ala
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Gly	Gly	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Lys	Asp	Asn		
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Val	Ala	Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr
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Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala
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Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly
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Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn
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Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu
											805				815
Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr
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Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala
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Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu

850	855	860
His Ser Leu Gln Asp	Leu Lys Ala Ser Pro	Gln Ala Lys Arg
865	870	875
Ser Val Ser Phe Ala His Tyr Cys	Glu Lys Glu Leu Asn	Leu Pro Ala
885	890	895
Val Leu Gly Val Ala Asn Gln	Ile Thr Arg Ala Leu	Leu Gly Val Glu
900	905	910
Ala His Glu Ile Ser Met Leu Phe	Leu Thr Asp Tyr Ile	Lys Ser Ala
915	920	925
Thr Gly Leu Ser Asn Ile Phe	Ser Asp Lys Lys Asp	Gly Gly Gln Tyr
930	935	940
Met Arg Cys Lys Thr Gly	Met Gln Ser Ile Cys	His Ala Met Ser Lys
945	950	955
Glu Leu Val Pro Gly Ser Val His	Leu Asn Thr Pro Val	Ala Glu Ile
965	970	975
Glu Gln Ser Ala Ser Gly Cys	Thr Val Arg Ser Ala	Ser Gly Ala Val
980	985	990
Phe Arg Ser Lys Lys Val Val	Ser Leu Pro Thr	Thr Leu Tyr Pro
995	1000	1005
Thr Leu Thr Phe Ser Pro Pro	Leu Pro Ala Glu	Lys Gln Ala Leu Ala
1010	1015	1020
Glu Asn Ser Ile Leu Gly Tyr	Tyr Ser Lys Ile Val Phe	Val Trp Asp
1025	1030	1035
Lys Pro Trp Trp Arg Glu Gln Gly	Phe Ser Gly Val	Leu Gln Ser Ser
1045	1050	1055
Cys Asp Pro Ile Ser Phe Ala Arg	Asp Thr Ser Ile Asp	Val Asp Arg
1060	1065	1070
Gln Trp Ser Ile Thr Cys Phe	Met Val Gly Asp Pro	Gly Arg Lys Trp
1075	1080	1085
Ser Gln Gln Ser Lys Gln Val Arg	Gln Lys Ser Val	Trp Asp Gln Leu
1090	1095	1100
Arg Ala Ala Tyr Glu Asn Ala Gly	Ala Gln Val Pro	Glu Pro Ala Asn
1105	1110	1115
Val Leu Glu Ile Glu Trp Ser Lys	Gln Gln Tyr Phe	Gln Gly Ala Pro
1125	1130	1135
Ser Ala Val Tyr Gly Leu Asn Asp	Leu Ile Thr Leu	Gly Ser Ala Leu
1140	1145	1150
Arg Thr Pro Phe Lys Ser Val His	Phe Val Gly	Thr Glu Thr Ser Leu
1155	1160	1165
Val Trp Lys Gly Tyr Met Glu	Gly Ala Ile Arg	Ser Gly Gln Arg Gly
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<212> DNA

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<223> GST:glyc(-)APAO open reading frame, 2490 nt; GST and linker, nt 1-687; Glyc (-) APAO, nt 688-2490; mutation in putative glycosylation sites in bold and underlined, nt 1288-1290 (AAT->TCC) and nt 1303-1305 (AGC->AAC).

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<221> misc_feature

<222> (1)...(687)

<223> GST and linker

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 <223> Glyc (-) APAO

<221> mutation
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 <223> mutation in putative glycosylation site (AAT->TCC)

<221> mutation
 <222> (1303)...(1305)
 <223> mutation in putative glycosylation site (AGC->AAC)

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act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg	96
Thr Arg Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu	
20 25 30	
tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg	144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu	
35 40 45	
ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa	192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys	
50 55 60	
tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac	240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn	
65 70 75 80	
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Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu	
85 90 95	
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Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser	
100 105 110	
aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa	384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu	
115 120 125	
atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat	432
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn	
130 135 140	
ggt gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat	480
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp	
145 150 155 160	
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Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu	
165 170 175	
gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac	576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr	
180 185 190	

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acc aag ctc aat tac tac atc gtc gac tac gcc ccg agc aaa ctc acc Thr Lys Leu Asn Tyr Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr 305 310 315 320	960
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aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg gag Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu 370 375 380	1152
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gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt ccc Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro 405 410 415	1248
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435	440	445	
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450	455	460	
aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val			1440
465	470	475	480
gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc gaa Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu			1488
485	490	495	
gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg ctc Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu			1536
500	505	510	
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515	520	525	
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530	535	540	
gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag agt Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser			1680
545	550	555	560
gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg cag Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln			1728
565	570	575	
tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg tca Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser			1776
580	585	590	
aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu			1824
595	600	605	
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610	615	620	
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625	630	635	640
ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu			1968
645	650	655	
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660	665	670	
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675	680	685	

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35	40	40	45	45		Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys		50	55	55	60	60		Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn		65	70	70	75	75	80	80		Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu		85	90	90	95	95		Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser		100	105	105	110	110		Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu		115	120	120	125	125		Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn		130	135	135	140	140		Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp																																																																																																																			
40	45	45		Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys		50	55	55	60	60		Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn		65	70	70	75	75	80	80		Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu		85	90	90	95	95		Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser		100	105	105	110	110		Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu		115	120	120	125	125		Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn		130	135	135	140	140		Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp																																																																																																																					
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Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys																																																																																																																																																																											
50	55	55	60	60		Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn		65	70	70	75	75	80	80		Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu		85	90	90	95	95		Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser		100	105	105	110	110		Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu		115	120	120	125	125		Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn		130	135	135	140	140		Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp																																																																																																																											
55	60	60		Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn		65	70	70	75	75	80	80		Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu		85	90	90	95	95		Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser		100	105	105	110	110		Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu		115	120	120	125	125		Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn		130	135	135	140	140		Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp																																																																																																																													
60																																																																																																																																																																											
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn																																																																																																																																																																											
65	70	70	75	75	80	80		Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu		85	90	90	95	95		Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser		100	105	105	110	110		Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu		115	120	120	125	125		Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn		130	135	135	140	140		Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp																																																																																																																																			
70	75	75	80	80		Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu		85	90	90	95	95		Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser		100	105	105	110	110		Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu		115	120	120	125	125		Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn		130	135	135	140	140		Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp																																																																																																																																					
75	80	80		Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu		85	90	90	95	95		Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser		100	105	105	110	110		Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu		115	120	120	125	125		Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn		130	135	135	140	140		Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp																																																																																																																																							
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Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu																																																																																																																																																																											
85	90	90	95	95		Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser		100	105	105	110	110		Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu		115	120	120	125	125		Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn		130	135	135	140	140		Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp																																																																																																																																													
90	95	95		Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser		100	105	105	110	110		Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu		115	120	120	125	125		Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn		130	135	135	140	140		Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp																																																																																																																																															
95																																																																																																																																																																											
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser																																																																																																																																																																											
100	105	105	110	110		Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu		115	120	120	125	125		Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn		130	135	135	140	140		Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp																																																																																																																																																					
105	110	110		Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu		115	120	120	125	125		Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn		130	135	135	140	140		Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp																																																																																																																																																							
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Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu																																																																																																																																																																											
115	120	120	125	125		Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn		130	135	135	140	140		Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp																																																																																																																																																													
120	125	125		Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn		130	135	135	140	140		Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp																																																																																																																																																															
125																																																																																																																																																																											
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn																																																																																																																																																																											
130	135	135	140	140		Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp																																																																																																																																																																					
135	140	140		Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp																																																																																																																																																																							
140																																																																																																																																																																											
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp																																																																																																																																																																											

145	150	155	160
Val	Val	Leu	Tyr
Met	Asp	Pro	Met
Cys		Leu	Asp
165		Ala	Phe
Val	Cys	Phe	Gly
Lys	Lys	Lys	Arg
180		Ile	Glu
Leu	Lys	Ser	Ser
185		Ala	Ile
190		Trp	Pro
195		Leu	Gln
200		Gly	Trp
205		Gln	Gly
Thr	Phe	Gly	Gly
210	Asp	His	Asp
Gly	Ser	Pro	Pro
225	Glu	Phe	Met
Asn	Val	Ala	Ser
230	Pro	Ala	Gly
245	250	Tyr	Tyr
Gly	Gly	Arg	Arg
260	265	Tyr	Val
Gly	Val	Thr	Asp
275	280	Ala	Pro
Asn	Leu	Arg	Ala
290	295	Cys	Gly
Thr	Lys	Leu	Asn
305	310	Ala	Tyr
Ala	Ile	Gly	Tyr
325	330	Asp	Val
Pro	Cys	Thr	Leu
340	345	Val	Val
Phe	Glu	Asp	Ala
355	360	Thr	Ala
Asn	Val	Ala	Asp
370	375	Val	Val
Thr	Ala	Arg	Lys
385	390	Val	Gln
Ala	Met	Asp	Arg
405	410	Val	Gly
Gly	Arg	Thr	Thr
420	425	Ile	Asn
Asn	Gln	Asn	Glu
435	440	Val	Val
Glu	Leu	Gln	Arg
450	455	Thr	Thr
Thr	Thr	Thr	Ala
465	470	Pro	Tyr
Ala	Ser	Ala	Leu
485	490	Glu	Leu
Glu	His	Ser	Leu
500	505	Gln	Asp
Asp	Ser	Val	Leu
515	520	Ser	Phe
Ala	Val	Leu	Gly
530	535	Val	Val
Glu	Ala	His	Glu
545	550	Ile	Ser
Ala	Thr	Gly	Leu
565	570	Leu	Ser
Tyr	Met	Arg	Cys
580	585	Lys	Thr
Lys	Glu	Leu	Val
595	600	Pro	Gly
Ile	Glu	Gln	Ser
610	615	Ala	Ser
Val	Phe	Arg	Ser
625	630	Lys	Val
Pro	Thr	Leu	Thr
		Phe	Asp
		Ser	Pro
		Pro	Leu
		Leu	Pro
		Pro	Ala
		Glu	Gly
		Gln	Ala
		Ala	Leu

645	650	655	
Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp			
660	665	670	
Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser			
675	680	685	
Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp			
690	695	700	
Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys			
705	710	715	720
Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln			
725	730	735	
Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala			
740	745	750	
Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala			
755	760	765	
Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala			
770	775	780	
Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser			
785	790	795	800
Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg			
805	810	815	
Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala			
820	825		